

Single-Cell Visualization with Minimum Volume Embedding

Authors : Zhenqiu Liu

Abstract : Visualizing the heterogeneity within cell-populations for single-cell RNA-seq data is crucial for studying the functional diversity of a cell. However, because of the high level of noises, outlier, and dropouts, it is very challenging to measure the cell-to-cell similarity (distance), visualize and cluster the data in a low-dimension. Minimum volume embedding (MVE) projects the data into a lower-dimensional space and is a promising tool for data visualization. However, it is computationally inefficient to solve a semi-definite programming (SDP) when the sample size is large. Therefore, it is not applicable to single-cell RNA-seq data with thousands of samples. In this paper, we develop an efficient algorithm with an accelerated proximal gradient method and visualize the single-cell RNA-seq data efficiently. We demonstrate that the proposed approach separates known subpopulations more accurately in single-cell data sets than other existing dimension reduction methods.

Keywords : single-cell RNA-seq, minimum volume embedding, visualization, accelerated proximal gradient method

Conference Title : ICMLB 2017 : International Conference on Machine Learning and Bioinformatics

Conference Location : Vancouver, Canada

Conference Dates : August 07-08, 2017